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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/922,488

DATE: 08/13/2001
 TIME: 11:25:00

Input Set : A:\0054.txt
 Output Set: N:\CRF3\08132001\I922488.raw

ENTERED

4 <110> APPLICANT: Thayer, Edward C.
 5 Webster, Philippa J.
 7 <120> TITLE OF INVENTION: Human Secreted Protein, Zzpl
 9 <130> FILE REFERENCE: 00-54
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/922,488
 C--> 11 <141> CURRENT FILING DATE: 2001-08-03
 11 <150> PRIOR APPLICATION NUMBER: 60/222,814
 12 <151> PRIOR FILING DATE: 2000-08-04
 14 <150> PRIOR APPLICATION NUMBER: 60/260,512
 15 <151> PRIOR FILING DATE: 2001-01-09
 17 <160> NUMBER OF SEQ ID NOS: 5
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1908
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)...(1908)
 30 <400> SEQUENCE: 1
 31 atg gca gga ggc tca gcc acg acc tgg ggt tac cct gtg gcc ctg cta 48
 32 Met Ala Gly Gly Ser Ala Thr Thr Trp Gly Tyr Pro Val Ala Leu Leu
 33 1 5 10 15
 35 ctg ctg gtt gcc acc ctg ggg ctg ggt agg tgg ctc cag ccc gac cca 96
 36 Leu Leu Val Ala Thr Leu Gly Leu Gly Arg Trp Leu Gln Pro Asp Pro
 37 20 25 30
 39 ggc ctc cgg cac agc tac gac tgt ggg atc aag gga atg cag ctg ctg 144
 40 Gly Leu Arg His Ser Tyr Asp Cys Gly Ile Lys Gly Met Gln Leu Leu
 41 35 40 45
 44 gtg ttc ccc agg cca ggc cag act ctc cgc ttc aag gtg gtg gat gaa 192
 45 Val Phe Pro Arg Pro Gly Gln Thr Leu Arg Phe Lys Val Val Asp Glu
 46 50 55 60
 48 ttt ggg aac cga ttt gat gtc aac aac tgc tcc atc tgc tac cac tgg 240
 49 Phe Gly Asn Arg Phe Asp Val Asn Asn Cys Ser Ile Cys Tyr His Trp
 50 65 70 75 80
 52 gtc acc tcc agg ccg cag gag cct gca gtc ttc tcg gcc gat tac aga 288
 53 Val Thr Ser Arg Pro Gln Glu Pro Ala Val Phe Ser Ala Asp Tyr Arg
 54 85 90 95
 56 ggc tgc cac gtg ctg gag aag gat ggg cgt ttc cac ctg agg gtg ttc 336
 57 Gly Cys His Val Leu Glu Lys Asp Gly Arg Phe His Leu Arg Val Phe
 58 100 105 110
 60 atg gag gct gtg ctg ccc aat ggt cgt gtg gat gtg gca caa gac gct 384
 61 Met Glu Ala Val Leu Pro Asn Gly Arg Val Asp Val Ala Gln Asp Ala
 62 115 120 125
 64 act ctg atc tgt ccc aaa cct gac ccc tcc cgg act ctg gac tcc cag 432
 65 Thr Leu Ile Cys Pro Lys Pro Asp Pro Ser Arg Thr Leu Asp Ser Gln
 66 130 135 140

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```

68 ctg gca cca ccc gcc atg ttc tct gtc tca acc cca caa acc ctt tcc 480
69 Leu Ala Pro Pro Ala Met Phe Ser Val Ser Thr Pro Gln Thr Leu Ser
70 145 150 155 160
72 ttc ctc ccc acc tct ggc cat acc tcc caa ggc tct ggc cat gcc ttt 528
73 Phe Leu Pro Thr Ser Gly His Thr Ser Gln Gly Ser Gly His Ala Phe
74 165 170 175
76 ccc agc cca ctg gac cca ggg cac agc tct gtc cac cca acc cct gct 576
77 Pro Ser Pro Leu Asp Pro Gly His Ser Ser Val His Pro Thr Pro Ala
78 180 185 190
80 tta cca tcc cct gga cct gga cct acc ctc gcc acc ctg gct caa ccc 624
81 Leu Pro Ser Pro Gly Pro Gly Pro Thr Leu Ala Thr Leu Ala Gln Pro
82 195 200 205
84 cac tgg ggc acc ttg gaa cac tgg gat gtg aac aaa cga gat tac ata 672
85 His Trp Gly Thr Leu Glu His Trp Asp Val Asn Lys Arg Asp Tyr Ile
86 210 215 220
88 ggt acc cac ctg agc cag gag cag tgc cag gtg gcc tca ggg cac ctc 720
89 Gly Thr His Leu Ser Gln Glu Gln Cys Gln Val Ala Ser Gly His Leu
90 225 230 235 240
92 ccc tgc atc gtg aga aga act tca aaa gaa gcc tgt cag cag gct ggc 768
93 Pro Cys Ile Val Arg Arg Thr Ser Lys Glu Ala Cys Gln Gln Ala Gly
94 245 250 255
96 tgc tgc tat gac aac acc aga gag gtt ccc tgt tac tat ggc aac aca 816
97 Cys Cys Tyr Asp Asn Thr Arg Glu Val Pro Cys Tyr Tyr Gly Asn Thr
98 260 265 270
100 gct act gtc cag tgc ttc aga gat ggc tac ttc gtc ctc gta gtg tcc 864
101 Ala Thr Val Gln Cys Phe Arg Asp Gly Tyr Phe Val Leu Val Val Ser
102 275 280 285
104 caa gaa atg gcc ttg aca cac agg atc aca ctg gcc aac atc cac ctg 912
105 Gln Glu Met Ala Leu Thr His Arg Ile Thr Leu Ala Asn Ile His Leu
106 290 295 300
108 gcc tat gcc ccc acc agc tgc tcc cca aca cag cac acg gaa gct ttc 960
109 Ala Tyr Ala Pro Thr Ser Cys Ser Pro Thr Gln His Thr Glu Ala Phe
110 305 310 315 320
112 gtg gtc ttc tac ttc cct ctc acc cac tgt gga acc aca atg cag gtg 1008
113 Val Val Phe Tyr Phe Pro Leu Thr His Cys Gly Thr Thr Met Gln Val
114 325 330 335
116 gct ggc gac cag ctc atc tat gag aac tgg ctg gtg tct ggc atc cac 1056
117 Ala Gly Asp Gln Leu Ile Tyr Glu Asn Trp Leu Val Ser Gly Ile His
118 340 345 350
120 atc caa aag ggg cca cag ggt tcc atc acg cgg gac agc acc ttc cag 1104
121 Ile Gln Lys Gly Pro Gln Gly Ser Ile Thr Arg Asp Ser Thr Phe Gln
122 355 360 365
124 ctt cat gtg cgc tgt gtc ttc aac gcc agt gac ttc ctg ccc att cag 1152
125 Leu His Val Arg Cys Val Phe Asn Ala Ser Asp Phe Leu Pro Ile Gln
126 370 375 380
129 gca tcc att ttc cca ccc cca tcg cct gct cct atg acc cag ccc ggc 1200
130 Ala Ser Ile Phe Pro Pro Ser Pro Ala Pro Met Thr Gln Pro Gly
131 385 390 395 400
133 ccc ctg cgg ctt gag ctg cgg att gcc aaa gac gag acc tgc agc tcg 1248

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```

134 Pro Leu Arg Leu Glu Leu Arg Ile Ala Lys Asp Glu Thr Cys Ser Ser
135          405          410          415
137 tac tat ggg gag gat gac tat ccc atc gtg agg ctg ctc cga gaa cca 1296
138 Tyr Tyr Gly Glu Asp Asp Tyr Pro Ile Val Arg Leu Leu Arg Glu Pro
139          420          425          430
141 gtc cat gtg gag gtc cgg ctt ctg cag agg aca gac ccc aac ctg gtc 1344
142 Val His Val Glu Val Arg Leu Leu Gln Arg Thr Asp Pro Asn Leu Val
143          435          440          445
145 ctg ctg ctg cac cag tgc tgg ggc gct ccc agt gcc aac ccc ttc cag 1392
146 Leu Leu Leu His Gln Cys Trp Gly Ala Pro Ser Ala Asn Pro Phe Gln
147          450          455          460
149 cag ccc cag tgg ccc atc ctg tca gac ggc tgc cct ttc aag ggc gac 1440
150 Gln Pro Gln Trp Pro Ile Leu Ser Asp Gly Cys Pro Phe Lys Gly Asp
151 465          470          475          480
153 agc tac aga acc caa atg gta gcc ttg gac ggg gcc aca cct ttc cag 1488
154 Ser Tyr Arg Thr Gln Met Val Ala Leu Asp Gly Ala Thr Pro Phe Gln
155          485          490          495
157 tcg cac tac cag cga ttc act gtt gct acc ttc gcc ctc ctg gac tca 1536
158 Ser His Tyr Gln Arg Phe Thr Val Ala Thr Phe Ala Leu Leu Asp Ser
159          500          505          510
161 ggc tcc cag aga gcc ctc aga gga ctg gtt tac ttg ttc tgc agc acc 1584
162 Gly Ser Gln Arg Ala Leu Arg Gly Leu Val Tyr Leu Phe Cys Ser Thr
163          515          520          525
165 tct gcc tgc cac acc tca ggg ctg gag act tgc tcc act gca tgt agc 1632
166 Ser Ala Cys His Thr Ser Gly Leu Glu Thr Cys Ser Thr Ala Cys Ser
167          530          535          540
169 act ggc act aca aga cag cga cga tcc tca ggt cac cgt aat gac act 1680
170 Thr Gly Thr Thr Arg Gln Arg Arg Ser Ser Gly His Arg Asn Asp Thr
171 545          550          555          560
173 gcc agg ccc cag gac atc gtg agc tct ccg ggg cca gtg ggc ttt gag 1728
174 Ala Arg Pro Gln Asp Ile Val Ser Ser Pro Gly Pro Val Gly Phe Glu
175          565          570          575
177 gat tct tat ggg cag gag ccc aca ctt ggg ccc aca gac tcc aat ggg 1776
178 Asp Ser Tyr Gly Gln Glu Pro Thr Leu Gly Pro Thr Asp Ser Asn Gly
179          580          585          590
181 aac tcc agc ctg aga cct ctc ctt tgg gcg gtc ctt ttg ctg cca gct 1824
182 Asn Ser Ser Leu Arg Pro Leu Leu Trp Ala Val Leu Leu Leu Pro Ala
183          595          600          605
185 gtt gcc ctg gtc ctt ggg ttt ggt gtc ttt gtg ggc ctg agc cag acc 1872
186 Val Ala Leu Val Leu Gly Phe Gly Val Phe Val Gly Leu Ser Gln Thr
187          610          615          620
189 tgg gcc cag aag ctc tgg gaa agc aac aga cag tga 1908
190 Trp Ala Gln Lys Leu Trp Glu Ser Asn Arg Gln *
191 625          630          635
194 <210> SEQ ID NO: 2
195 <211> LENGTH: 635
196 <212> TYPE: PRT
197 <213> ORGANISM: Homo sapiens
199 <400> SEQUENCE: 2

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```

200 Met Ala Gly Gly Ser Ala Thr Thr Trp Gly Tyr Pro Val Ala Leu Leu
201 1 5 10 15
202 Leu Leu Val Ala Thr Leu Gly Leu Gly Arg Trp Leu Gln Pro Asp Pro
203 20 25 30
204 Gly Leu Arg His Ser Tyr Asp Cys Gly Ile Lys Gly Met Gln Leu Leu
205 35 40 45
206 Val Phe Pro Arg Pro Gly Gln Thr Leu Arg Phe Lys Val Val Asp Glu
207 50 55 60
208 Phe Gly Asn Arg Phe Asp Val Asn Asn Cys Ser Ile Cys Tyr His Trp
209 65 70 75 80
210 Val Thr Ser Arg Pro Gln Glu Pro Ala Val Phe Ser Ala Asp Tyr Arg
211 85 90 95
212 Gly Cys His Val Leu Glu Lys Asp Gly Arg Phe His Leu Arg Val Phe
213 100 105 110
215 Met Glu Ala Val Leu Pro Asn Gly Arg Val Asp Val Ala Gln Asp Ala
216 115 120 125
217 Thr Leu Ile Cys Pro Lys Pro Asp Pro Ser Arg Thr Leu Asp Ser Gln
218 130 135 140
219 Leu Ala Pro Pro Ala Met Phe Ser Val Ser Thr Pro Gln Thr Leu Ser
220 145 150 155 160
221 Phe Leu Pro Thr Ser Gly His Thr Ser Gln Gly Ser Gly His Ala Phe
222 165 170 175
223 Pro Ser Pro Leu Asp Pro Gly His Ser Ser Val His Pro Thr Pro Ala
224 180 185 190
225 Leu Pro Ser Pro Gly Pro Gly Pro Thr Leu Ala Thr Leu Ala Gln Pro
226 195 200 205
227 His Trp Gly Thr Leu Glu His Trp Asp Val Asn Lys Arg Asp Tyr Ile
228 210 215 220
229 Gly Thr His Leu Ser Gln Glu Cys Gln Val Ala Ser Gly His Leu
230 225 230 235 240
231 Pro Cys Ile Val Arg Arg Thr Ser Lys Glu Ala Cys Gln Gln Ala Gly
232 245 250 255
233 Cys Cys Tyr Asp Asn Thr Arg Glu Val Pro Cys Tyr Tyr Gly Asn Thr
234 260 265 270
235 Ala Thr Val Gln Cys Phe Arg Asp Gly Tyr Phe Val Leu Val Val Ser
236 275 280 285
237 Gln Glu Met Ala Leu Thr His Arg Ile Thr Leu Ala Asn Ile His Leu
238 290 295 300
239 Ala Tyr Ala Pro Thr Ser Cys Ser Pro Thr Gln His Thr Glu Ala Phe
240 305 310 315 320
241 Val Val Phe Tyr Phe Pro Leu Thr His Cys Gly Thr Thr Met Gln Val
242 325 330 335
243 Ala Gly Asp Gln Leu Ile Tyr Glu Asn Trp Leu Val Ser Gly Ile His
244 340 345 350
245 Ile Gln Lys Gly Pro Gln Gly Ser Ile Thr Arg Asp Ser Thr Phe Gln
246 355 360 365
247 Leu His Val Arg Cys Val Phe Asn Ala Ser Asp Phe Leu Pro Ile Gln
248 370 375 380
249 Ala Ser Ile Phe Pro Pro Pro Ser Pro Ala Pro Met Thr Gln Pro Gly

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```

250 385          390          395          400
251 Pro Leu Arg Leu Glu Leu Arg Ile Ala Lys Asp Glu Thr Cys Ser Ser
252          405          410          415
253 Tyr Tyr Gly Glu Asp Asp Tyr Pro Ile Val Arg Leu Leu Arg Glu Pro
254          420          425          430
255 Val His Val Glu Val Arg Leu Leu Gln Arg Thr Asp Pro Asn Leu Val
256          435          440          445
258 Leu Leu Leu His Gln Cys Trp Gly Ala Pro Ser Ala Asn Pro Phe Gln
259          450          455          460
260 Gln Pro Gln Trp Pro Ile Leu Ser Asp Gly Cys Pro Phe Lys Gly Asp
261 465          470          475          480
262 Ser Tyr Arg Thr Gln Met Val Ala Leu Asp Gly Ala Thr Pro Phe Gln
263          485          490          495
264 Ser His Tyr Gln Arg Phe Thr Val Ala Thr Phe Ala Leu Leu Asp Ser
265          500          505          510
266 Gly Ser Gln Arg Ala Leu Arg Gly Leu Val Tyr Leu Phe Cys Ser Thr
267          515          520          525
268 Ser Ala Cys His Thr Ser Gly Leu Glu Thr Cys Ser Thr Ala Cys Ser
269          530          535          540
270 Thr Gly Thr Thr Arg Gln Arg Arg Ser Ser Gly His Arg Asn Asp Thr
271 545          550          555          560
272 Ala Arg Pro Gln Asp Ile Val Ser Ser Pro Gly Pro Val Gly Phe Glu
273          565          570          575
274 Asp Ser Tyr Gly Gln Glu Pro Thr Leu Gly Pro Thr Asp Ser Asn Gly
275          580          585          590
276 Asn Ser Ser Leu Arg Pro Leu Leu Trp Ala Val Leu Leu Leu Pro Ala
277          595          600          605
278 Val Ala Leu Val Leu Gly Phe Gly Val Phe Val Gly Leu Ser Gln Thr
279          610          615          620
280 Trp Ala Gln Lys Leu Trp Glu Ser Asn Arg Gln
281 625          630          635
284 <210> SEQ ID NO: 3
285 <211> LENGTH: 1905
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: degenerate nucleotide sequence
292 <221> NAME/KEY: misc_feature
293 <222> LOCATION: 6, 9, 12, 15, 18, 21, 24, 30, 36, 39, 42, 45, 48, 51, 54,
294          57, 60, 63, 66, 69, 72, 75, 78, 84, 90, 96, 99, 102, 105,
295          111, 123, 132, 141, 144, 147, 153, 156, 159, 162, 168, 171,
296          174, 183, 186, 198, 204, 213, 225, 243, 246, 249, 252
297 <223> OTHER INFORMATION: n = A,T,C or G
299 <221> NAME/KEY: misc_feature
300 <222> LOCATION: 255, 264, 267, 270, 276, 279, 288, 291, 300, 303, 315, 318,
301          327, 330, 333, 345, 348, 351, 354, 360, 363, 366, 372, 375,
302          384, 387, 390, 399, 405, 411, 414, 417, 420, 423, 429, 435,
303          438, 441, 444, 447, 456, 459, 462, 465, 468, 474, 477
304 <223> OTHER INFORMATION: n = A,T,C or G

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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DATE: 08/13/2001

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Input Set : A:\0054.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3